

6500922

	Preimmune	Anti-mTNF-R2	Preimmune	Anti-mTNF-R2	Preimmune	Anti-mTNF-R2	Preimmune	Anti-mTNF-R2
NF- κ B Probe	wt	wt	mt	mt	wt	wt	wt	wt
Competitor	-	-	-	-	mt	mt	AP-1	

B ▶

F ▶

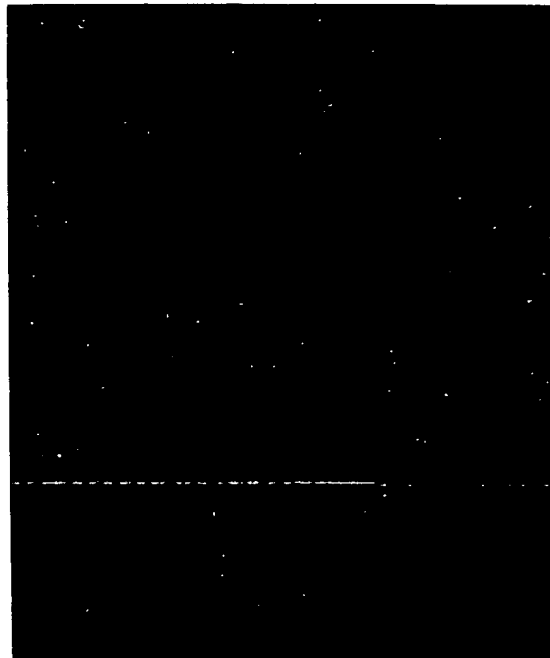


FIG. 1

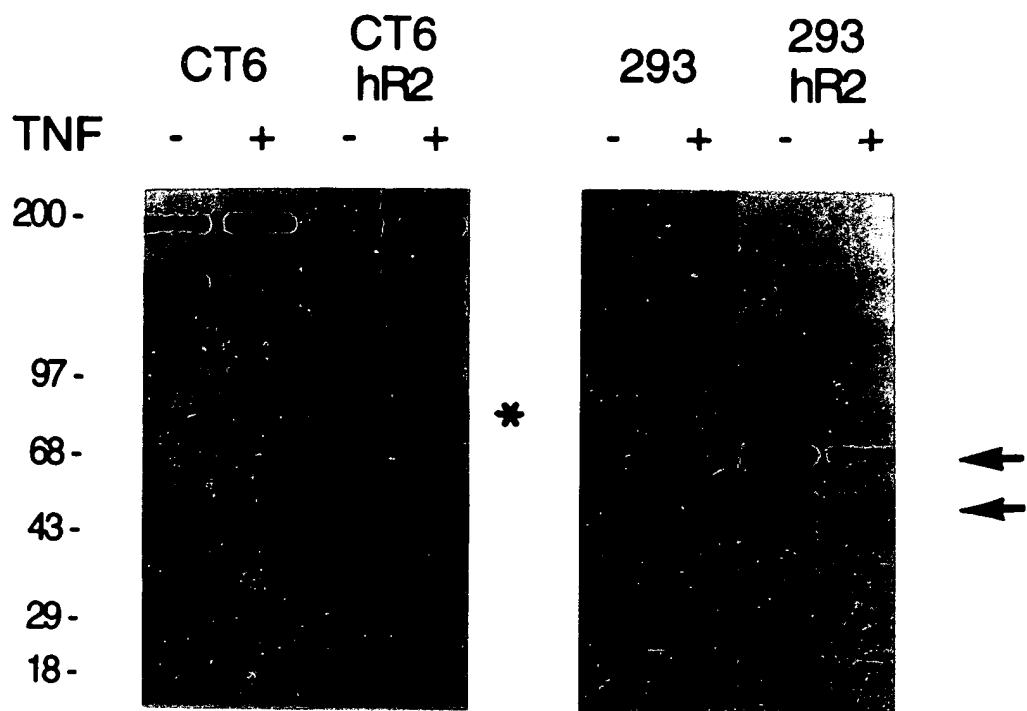


FIG. 2a

CT6
FIG. 2b



FIG. 3

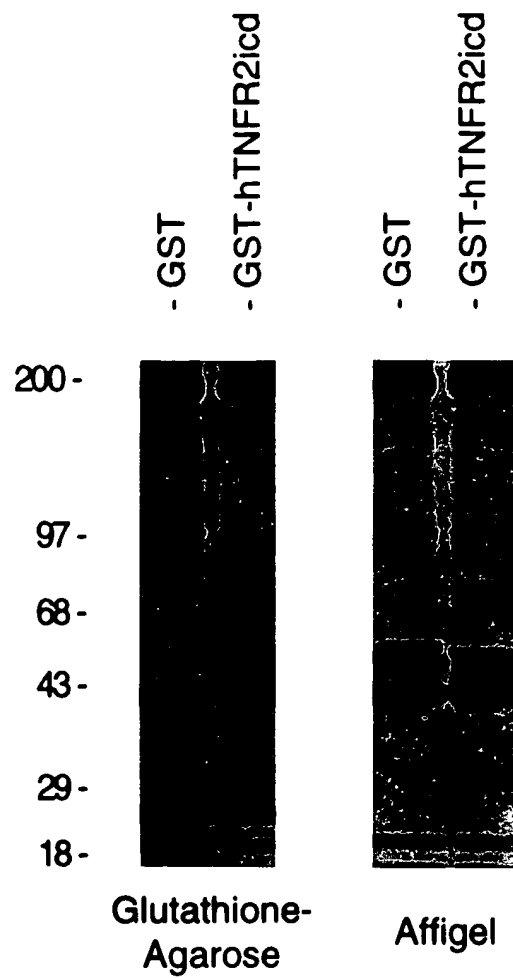


FIG. 4

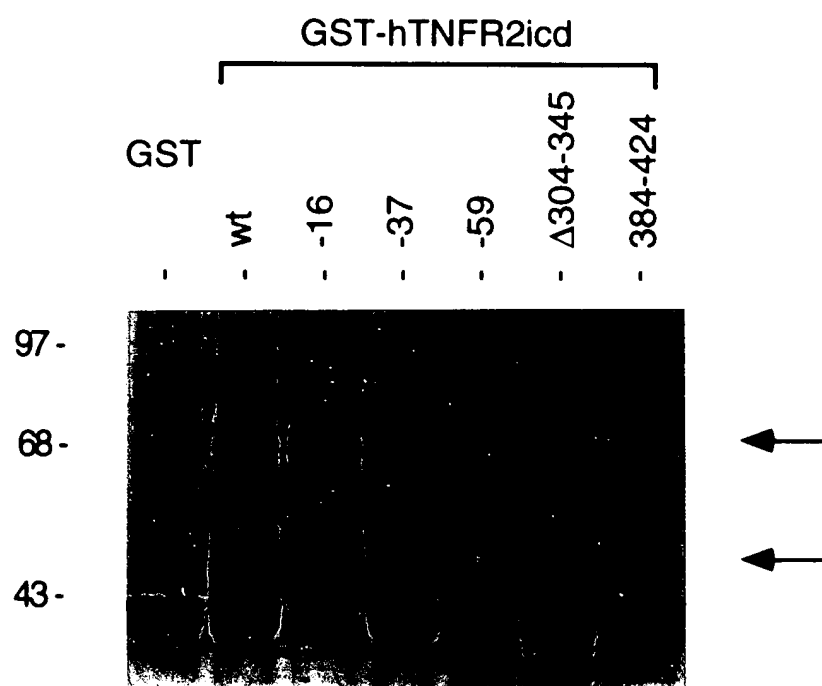


FIG. 5

	293			293-hR2				
Competitor	-	GST	wt	-	GST	wt	GST-hTNFR2icd -16 -37 -59	
	

FIG. 6a

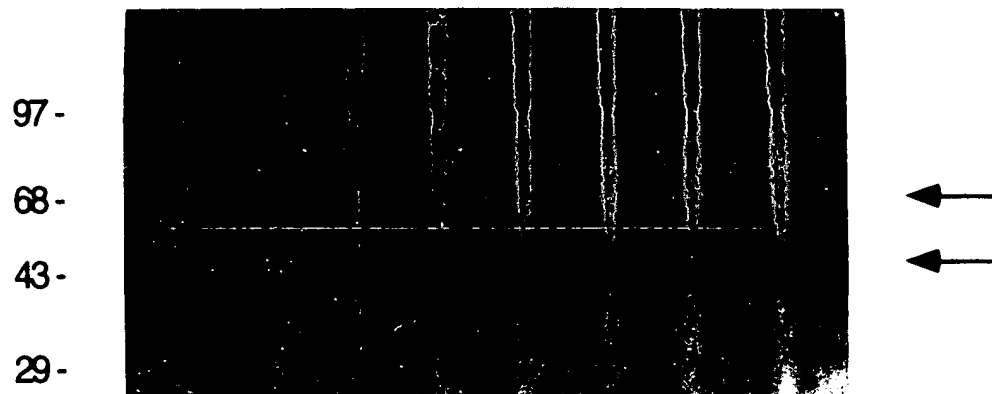


FIG. 6b



CT6

	GST		GST-hTNFR2icd	
TNF	-	+	-	+

FIG. 7



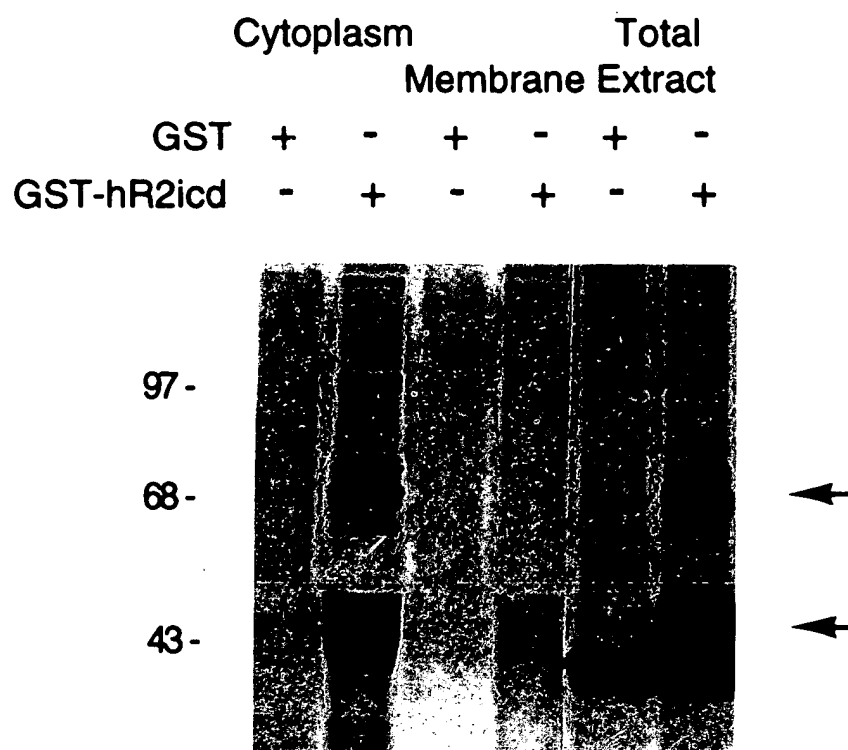


FIG. 8

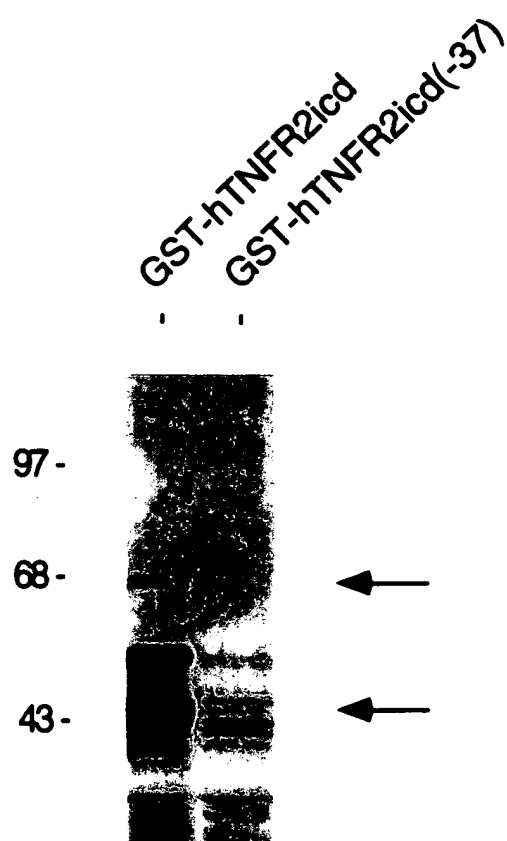


FIG. 9

1 CCCAGCCCGGTTCTCTGCCCCCAAGGACGGCTACCGCCCAATGCGAGCAGAAGGCGGCACAGATACAGAAAGT
74 GAGGCTCAGACATATTGAAGACCGTGTGACATAGGGTAGCCAAATGACAGTGTGAGAAAGTGACATTTACTCAAG
149 GCCACCCAGATATCCTGGAGGACCCAGAACCTGGAGATTCCCATCAGAAAGACCCTTCTG6CCACCIGAAACCCC

1 MetAlaSerSerSerAlaProAspGluAsnGluPheGlnPheGlyCysProProAlaProCysGlnAspPro
224 AAGATGGCCTCCAGCTCAGCCCTGATGAAACGAGTTTCAATTTGGTTGCCCCCTGCTCCCTGCCAGGACCCCA

25 SerGluProArgValLeuCysCysThrAlaCysLeuSerGluAsnLeuArgAspGluAspArgIleCysPro
299 TCGGAGCCACAGATTCTCTGCTGCACAGCCTGTCTCTGAGAACCTGAGAGATGATGAGGATCGGATCTGTCTCT

50 LysCysArgAlaAspAsnLeuHisProValSerProGlySerProLeuThrGlnGluLysValHisSerAspVal
374 AAATGCAGAGCAGACAACCTCCATCCTGTGAGCCCAGGAAGCCCTCTGACTCAGGAGAAGGTTCACTCTGATGTA

75 AlaGluAlaGluIleMetCysProPheAlaGlyValGlyCysSerPheLysGlySerProGlnSerMetGlnGlu
449 GCTGAGGCTGAAATCATGTGCCCTTTTGCAGGTGTGGCTGTTCCCTTCAAGGGGAGCCACCAATCCATGCAGGAG

100 HisGluAlaThrSerGlnSerSerHisLeuTyrLeuLeuLeuAlaValLeuLysGluTrpLysSerSerProGly
524 CATGAGGCTACCTCCCAGTCTCCACCTGTACCTGTCTGGCGGCTTAAAGGAGTGGAAATCCTCACCAGGC

125 SerAsnLeuGlySerAlaProMetAlaLeuGluArgAsnLeuSerGluLeuGlnLeuGlnAlaAlaValGluAla
599 TCCAAACCTAGGGTCTGCACCCATGGCACTGGAGCGGAACCTGTTCAGAGCTGCAGCTTCAGGCAGCTGTGGAAAGCG

150 ThrGlyAspLeuGluValAspCysTyrArgAlaProCysCysGluSerGlnGluGluLeuAlaLeuGlnHisLeu
674 ACAGGGGACCTGGAGGTAGACTGCTACCGGGCACCTTGCTGTGAGAGCCAGGAAGAACTGGCCCTGCAGCACTTG

> +
175 ValLysGluLysLeuLeuAlaGlnLeuGluGluLysLeuArgValPheAlaAsnIleValAlaValLeuAsnLys
749 GTGAAGGAGAAGCTGTGGCTCAGCTGGAGGAGAAGCTGCGTGTGTTTGCAACAATTGTGCTGTCTCAACAAG

200 GluValGluAlaSerHisLeuAlaLeuAlaAlaSerIleHisGlnSerGlnLeuAspArgGluHisLeuLeuSer
824 GAAGTGGAGGCTTCCACCTGGCAGCTGGCCGCCTCCATCCACCAGAGCCAGTTGGACCAGAGCACCCTCCTGAGC

225 LeuGluGlnArgValValGluLeuGlnGlnThrLeuAlaGlnLysAspGlnValLeuGlyLysLeuGluHisSer
899 TTGGAGCAGAGGGTGGTGGAAATTACAGCAAAACCCCTGGCTCAAAAAGACCAGGTCTCTGGGCAAGCTTGAGCACAGT

FIG. 10a

250 LeuArgLeuMetGluGluAlaSerPheAspGlyThrPheLeuTrpLysIleThrAsnValThrLysArgCysHis
 974 CTGCGACTCATGGAGGAGGCATCCTTTGATGGTACTTTCCCTGTGGAGATCACCAATGTACCAAGCGGTGCCAC

 275 GluSerValCysGlyArgThrValSerLeuPheSerProAlaPheIyrThrAlaLysIyrGlyIyrLysLeuCys
 1049 GAGTCAGTGTGTGGCCGGACTGTACGCCCTCTCTCTCCAGCTTTCTACACTGCCAAGTATGGTTACAAGTTGTGC

 300 LeuArgLeuIyrLeuAsnGlyAspGlySerGlyLysLysThrHisLeuSerLeuPheIleValIleMetArgGly
 1124 CTGCGCTTGTACCTGAACGGGGATGGCTCAGGCAAGAACCCACCTGTCCCTCTTCATCGTGATCATGAGAGGA

 325 GluTyrAspAlaLeuLeuProTrpProPheArgAsnLysValThrPheMetLeuLeuAspGlnAsnAsnArgGlu
 1199 GAATACGATGCTCTCTGCCCTGGCCTTTCAGGAACAAGGTCACTTTATGTCTACTTGACCAGAACAAACCGAGAG

 350 HisAlaIleAspAlaPheArgProAspLeuSerSerAlaSerPheGlnArgProGlnSerGluThrAsnValAla
 1274 CATGCTATTGATGCCCTCCGGCCTGACCTGAGCTCAGCCTCCTTCCAGCGGCCACAGAGTGAGACCAACGTGGCC

 375 SerGlyCysProLeuPhePheProLeuSerLysLeuGlnSerProLysHisAlaTyrValLysAspAspThrMet
 1349 AGCGGCTGCCCGCTCTTCTTCCCCCTCAGCAAGCTGCAGTCACCCCAAGCACGCTACGTCAAAGATGACACAATG

 <
 400 PheLeuLysCysIleValAspThrSerAla
 1424 TTCCTCAATGCATTGTGGACACTAGTGTCTTAGGGATGGGGGGAGGGGGTGTCTCTTGACAGAACCCAGCTTAGAC
 1499 TGGGGGACTTAGCTAGACAGCCAGGCCCTGCTGCCCTTGAGGCCACAGCCACGACCAAGGAGGAGCCAAAGGCT
 1574 GGCA TGACTTCAGCGCCACAGCATGTCTGGTTATGGCTGATGTGAGGCTGGAGAAACGTGTGCGTACAGAGACAGA
 1649 GTGGAGGAGACAGAGAGTGCTCTTTTCAACACAGACTACAGACACCGAGGAGGCCAGCATGCCAGCAGCTTCTG
 1724 AATGTTGAGACCGCCTAGATCAGGATGAAGAGCCAGGCCCTGAGGCTTGGACATTGAGCCAAAGGCTATGGGGC
 1799 CTAA GTGGAGGGCACTCTACCAAGGACATTCTCTCGAGGTCAAGGCATAACTGGAAATAAGCCCTCTCTCT
 1874 GTTCAGACTCAAAACTAGAACCAAGGAGGTCAGACATTAAATGTGAATTTAACTTGCCTGGACTGAGT
 1949 TCCTATGTTAACAGACACGCAACAGGTAAACCCAGAACTGCCCTGGGAAATGCTTTCTGGCTGCATCTGGAGA
 2024 TCTTTGATGTTTTTACCGACAAACAAATAACAAAGCCTTGAA TTGCAAAAAAATAAAAAA

FIG. 10b

285 I l e v a l C y s v a l l e u A s n A r g G l u V a l G l u A r g V a l A l a V a l T h r A l a G l u A l a C y s S e r A r g G l n H i s A r g L e u
900 A T T G T C T G C G T C T T G A A C C G T G A A G T A G A G G G T A G C A G T G A C T G C A G A G G C T T G T A G C C G G C A G C A C C G G C T A
310 A s p G l n A s p L y s I l e G l u A l a L e u S e r A s n L y s V a l G l n G l n L e u G l u A r g S e r I l e G l y L e u L y s A s p L e u A l a
975 G A C C A G G A C A A G A T T G A G G C C C T G A G T A A C A A G G T G C A A C A G C T G G A G A G G A G C A T C G G C C T C A A G G A C C T G G C C
335 M e t A l a A s p L e u G l u G l n L y s V a l S e r G l u L e u G l u V a l S e r T h r T y r A s p G l y V a l P h e I l e T r p L y s I l e S e r
1050 A T G G C T G A C C T G G A G C A G A A G G T C T C C G A G T T G G A A G T A T C C A C C T A T G A T G G G T C T T C A T C T G G A A G A T C T C T
360 A s p P h e T h r A r g L y s A r g G l n G l u A l a V a l A l a G l y A r g T h r P r o A l a I l e P h e S e r P r o A l a P h e T y r T h r S e r
1125 G A C T T C A C C A G A A A G C G T C A G G A A G C C G T A G T G C C G G A C A C C A G C T A T C T T C T C C C C A G C C T T C T A C A C A A G C
385 A r g T y r G l y T y r L y s M e t C y s L e u A r g V a l T y r L e u A s n G l y A s p G l y T h r G l y A r g G l y T h r H i s L e u S e r L e u
1200 A G A T A T G G C T A C A A G A T G T G T C T A C G A G T C T A C T T G A A T G G C G A C G G C A C T G G G C G G G A A C T C A T C T G T C T C T C
410 P h e P h e V a l V a l M e t L y s G l y P r o A s n A s p A l a L e u L e u G l n T r p P r o P h e A s n G l n L y s V a l T h r L e u M e t L e u
1275 T T C T T C G T G G T G A T G A A A G G C C C A A T G A T G T C T G T T G C A G T G G C C T T T T A A T C A G A A G G T A A C A T T G A T G T T G
435 L e u A s p H i s A s n A r g G l u H i s V a l I l e A s p A l a P h e A r g P r o A s p V a l T h r S e r S e r P h e G l n A r g P r o
1350 C T G G A C C A T A A C A C C G G G A G C A T G T G A T C G A C G C A T T C A G G C C C G A T G T A A C C T C G T C C T C C T T C C A G A G G C C T
460 V a l S e r A s p M e t A s n I l e A l a S e r G l y C y s P r o L e u P h e C y s P r o V a l S e r L y s M e t G l u A l a L y s A s n S e r T y r
1425 G T C A G T G A C A T G A A C A T C G C C A G T G G C T G C C C C C T C T T C T G C C C T G T G T C C A A G A T G G A G G C C A A G A A T T C C T A T
485 V a l A r g A s p A l a I l e P h e I l e L y s A l a I l e V a l A s p L e u T h r G l y L e u
1500 G T G C G G G A T G A T G C G A T C T T C A T C A A A G C T A T T G T G G A C C T A A C A G G A C T C T A G C C A C C C C T G C T A A G A A T A G C A
1575 G C T C A G T G A G G A G C T G T C A C A T T A G G C C A G C C A G G C C T G C C A C A C A C A C A G G T G G G C A G G C T T G G T G T A A A T G C T G
1650 G G G A G G C C T C A G C C T A G A G C C A A T C A C C A T C A C A C A G A A A G G C A G G A A G A A G C C T C C A G T T G G C C T T C A G C T G G
1725 C A A C T G A G T T G A C G G T C C A C T G A G C T C A A G G C C T G G T G G A G C C G C T G G G A G C T T C T C A G C T T T C C A A T A G
1800 G A A G C T C C T G C T G T C T G T C T G G G A A G G A G A G A C C T G T A G T G G G T G C T A G A A A G G G C C T C T C C A G A
1875 G A G A G T C T C A A G A G C T G C A G C A G G A A A G T A C T G G C C T T C C C C A C C C C A T C C T T G G A A A A G A G G T A G C G G C
1950 T A C A C A G G A A A G G C A T G C G C C T G C A G G G T G T A G C C C A A G A G A A G C T C T C T G A G A C A T A G G C C C T C A C T G G A G
2025 A A G G C C T G C C T G G G C T G C A C A G C C T T G C C A G G T G C C T G T A T G G G G G A G A A G T G A T T A A A T G T T G A G A T G T C A C
2100 A C G A C A A A A A A A A A A A A A A A A

FIG. 11b

FIG. 12a

TRAF2	(mouse)	31	KYL C SACKNILRRPFQA Q CGH RY C SF C LTSI	LSS	GPQN C AA C VYE
COP1	(<i>A. thaliana</i>)	49	DLL C PI C MQIIKDAFLT A CGH SF C YM C IITH	LRN	KSD C Pc C SQH
EPF	(human)	10	ELS C SI C LEPFKEPVT P CGH NF C GS C LNETWA VQG	SPYL C PQ C RAV	
RAD-18	(<i>S. cerevisiae</i>)	25	LLR C Hi C KDFLKVPLT P CGH Tf C SL C IRTH	LNN	QPN C PL C LFE
UVS-2	(<i>N. crassa</i>)	31	AFR C HV C KDFYDSPMLT S CNH Tf C SL C IRRC	LSV DSK	C PL C CRAT
RAG-1	(human)	290	SIS C QI C EHILADPVET N CKH Vf C RV C ILRC	LKV	MGSY C P C S C RYP
SS-A/Ro	(human)	13	EVT C PI C LDPFVEPVS I E CGH Sf C QE C ISQV	GKG	GGSV C AV C RQR
RING1	(human)	16	ELM C PI C LDMLKNTMTTKE C LH R f C SD C IVTA	LRS	GNKE C Pt C RRK
RPT-1	(mouse)	12	EVT C PI C LELLKEPVS A D CNH Sf C RA C ITLNYESNRNTDGKGN C PV C RV		
RFP	(human)	13	ETT C PV C LQYFAEPMML D CGH NI C CA C LARCWGTA	ETNV S C PQ C RET	
c-cbl	(human)	378	FQL C KI C AENDKDKIE P CGH LM C T S CLTS WQESEGQ	GSSG C PF C RCE	
consensus			<div> <div>X11-12</div> <div> <div>-----C-H-C-----</div> <div>-----C-----</div> </div> </div> <div> <div>X10-16</div> <div> <div>-----C-----</div> <div>-----C-----</div> </div> </div>		

FIG. 12b

TRAF2	(mouse)	157	CPKRSLS C QH C RAPCSHVDLEV H YE V C
		182	PKFPLT C DG C GKKKIPRET F QD H VR A C
DG17	(<i>D. discoideum</i>)	171	GGFKLVT C DF C KRDDIKKKELET H YK T C
TFIIIA	(<i>X. laevis</i>)	189	QD LAV C DV C NRKFRHKDYLRD H QK T H
XLCOF14	(<i>X. laevis</i>)	1	TGKYPFI C SE C GKSFMDKRYLKI H SN V H
XFIN	(<i>X. laevis</i>)	1225	TGEKPYT C TV C GKKFIDRSSVVK H SR T H
ZFY1/2	(mouse)	521	RKKFPHI C GE C GKGFRHPSALKK H IR V H
MFG2	(mouse)	293	SEEKPF E CE E C G KKFRTARHLVK H QR I H
RAD18	(<i>S. cerevisiae</i>)	183	PNEQMAQ C PI C QQFYPLKALEKT H LD E C
UVS-2	(<i>N. crassa</i>)	182	PDDGLVA C PI C LTRM KEQQVDR H LDT S C

TRAF2 1 M A A A S V T S P G S L E L L O P G F S K T L L G T R L E A K Y L C S A C K N I L R R P F Q A Q C G
 TRAF2 51 H R Y C S F C L T S I L S S G P Q N C A A C V Y E G L Y E E G I S I L E S S S A F P D N A A R R E V
 TRAF2 101 E S L P A V C P N D G C T W K G T L K E Y E S C H E G L C P F L L T E C P A C K G L V R L S E K E H
 TRAF1 1 M A S S S A P D E N E F Q F G C P P A
 TRAF2 151 H T E Q E C P K R S L S C Q H C R A P C S H V D L E V H Y E V C P K F P L T C D G C G K K K I P R E
 TRAF1 20 P C O D P S E P R V L C C T A C L S E N L R D D E D R I C P K C R A D N L H P V S P G S P L T Q E
 TRAF2 201 T F Q D H V R A C S K C R V L C R F H T V G C S E M V E T E N L Q D H E L Q R L R E H L A L L L S S
 TRAF1 69 K V H S D V . . . A E A E I M C P F A G V G C S F K G S P Q S M Q E H E A T S Q S S H L Y L L L A V
 TRAF2 251 F L E A Q A S P G T L N Q V G P E L L Q R
 TRAF1 116 L K E W K S S P G S N L G S A P M A L E R N L S E L Q L Q A A V E A T G D L E V D C Y R A P C C E S
 TRAF2 272 C Q I L E Q K I A T F E N I V C V L N R E V E R V A V T A E A C S R Q H
 TRAF1 166 G E E L A L O H L V K E K L L A Q L E E K L R V F A N I V A V L N K E V E A S H L A L A A S I H Q S
 TRAF2 308 R L D Q D K I E A L S N K V Q Q L E R S I G L K D L A M A D L E Q K V S E L E V S T Y D G V F I W K
 TRAF1 216 Q L D R E H L L S L E Q R V V E L Q O T L A Q K D Q V L G K L E H S L R L M E E A S F D G T F L W K
 TRAF2 358 I S D F T R K R Q E A V A G R T P A I F S P A F Y T S R Y G Y K M C L R V Y L N G D G T G R G T H L
 TRAF1 266 I T N V T K R C H E S V C G R T V S L F S P A F Y T A K Y G Y K L C L R L Y L N G D G S G K K T H L
 TRAF2 408 S L F F V V M K G P N D A L L Q W P F N Q K V T L M L L D H N N R E H V I D A F R P D V T S S S F Q
 TRAF1 316 S L F I V I M R G E Y D A L L P W P F R N K V T F M L L D Q N N R E H A I D A F R P D L S S A S F Q
 TRAF2 458 R P V S D M N I A S G C P L F C P V S K M E . A K N S Y V R D D A I F I K A I V D L T G L
 TRAF1 366 R P O S E T N V A S G C P L F F P L S K L Q S P K H A Y V K D D T M F L K C I V D T S A

FIG. 13

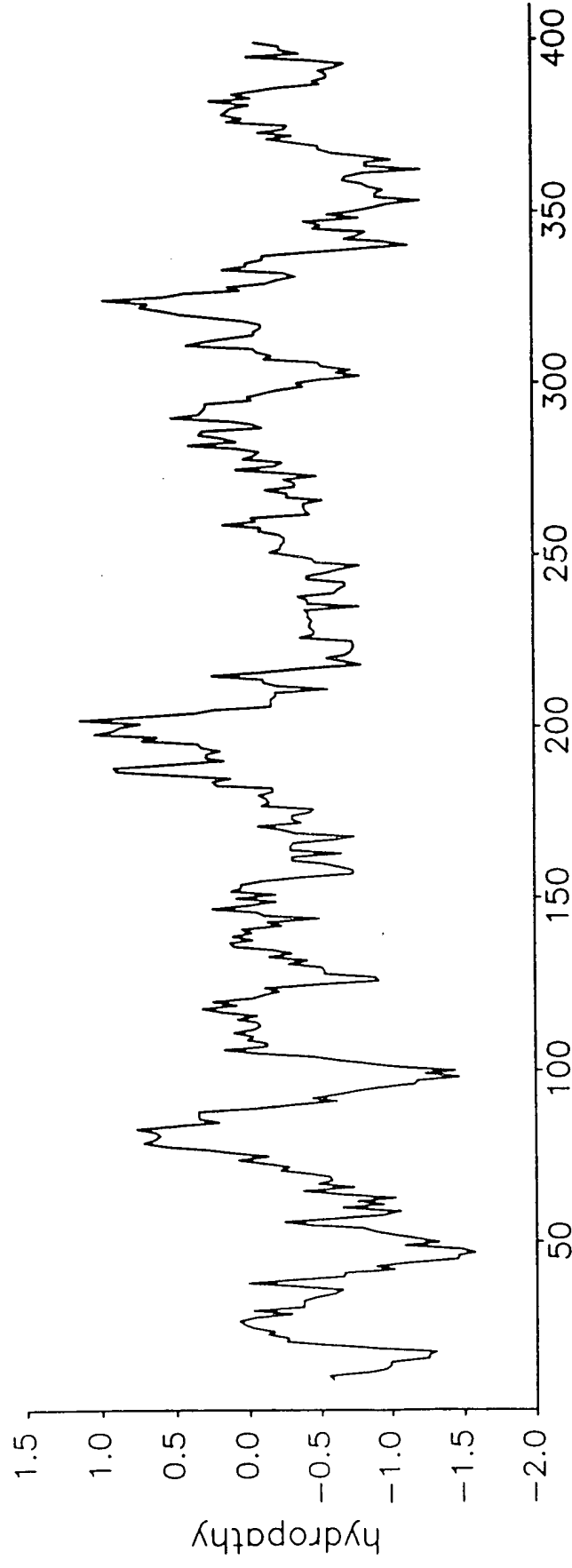


FIG. 14a

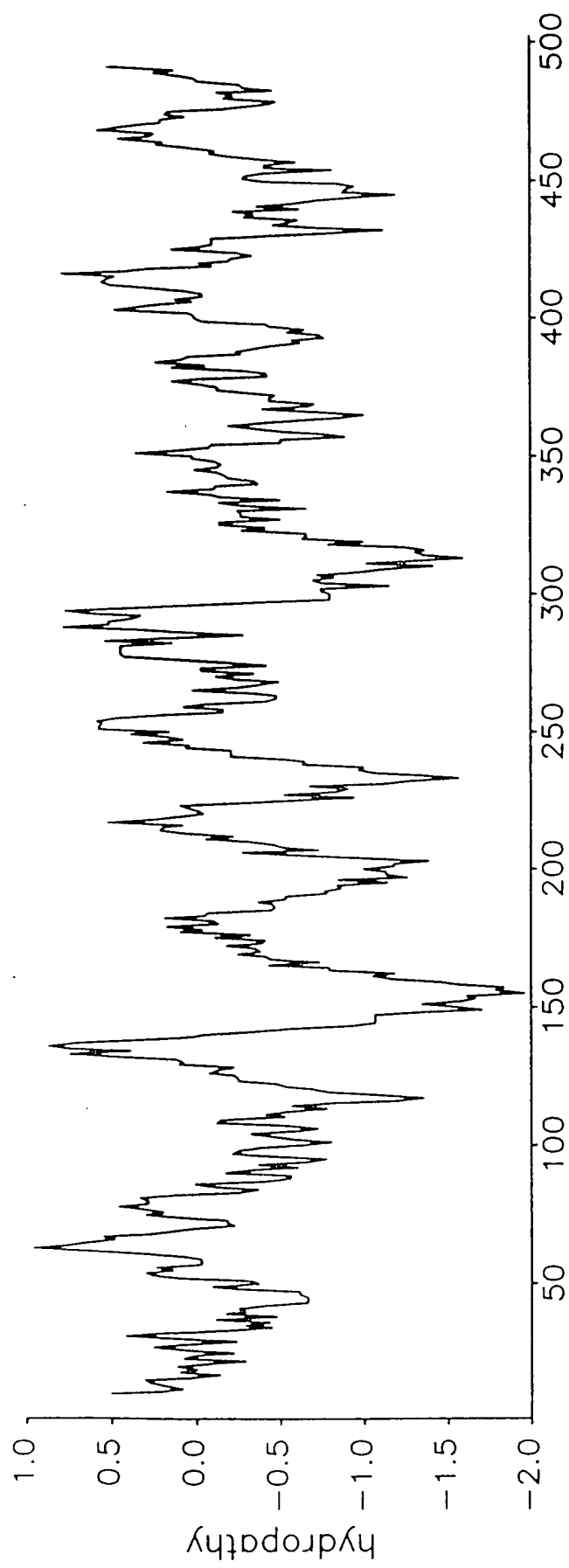


FIG. 14b

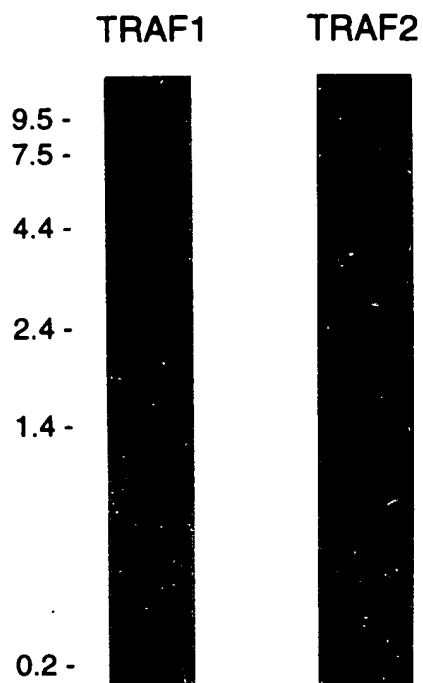


FIG. 15a

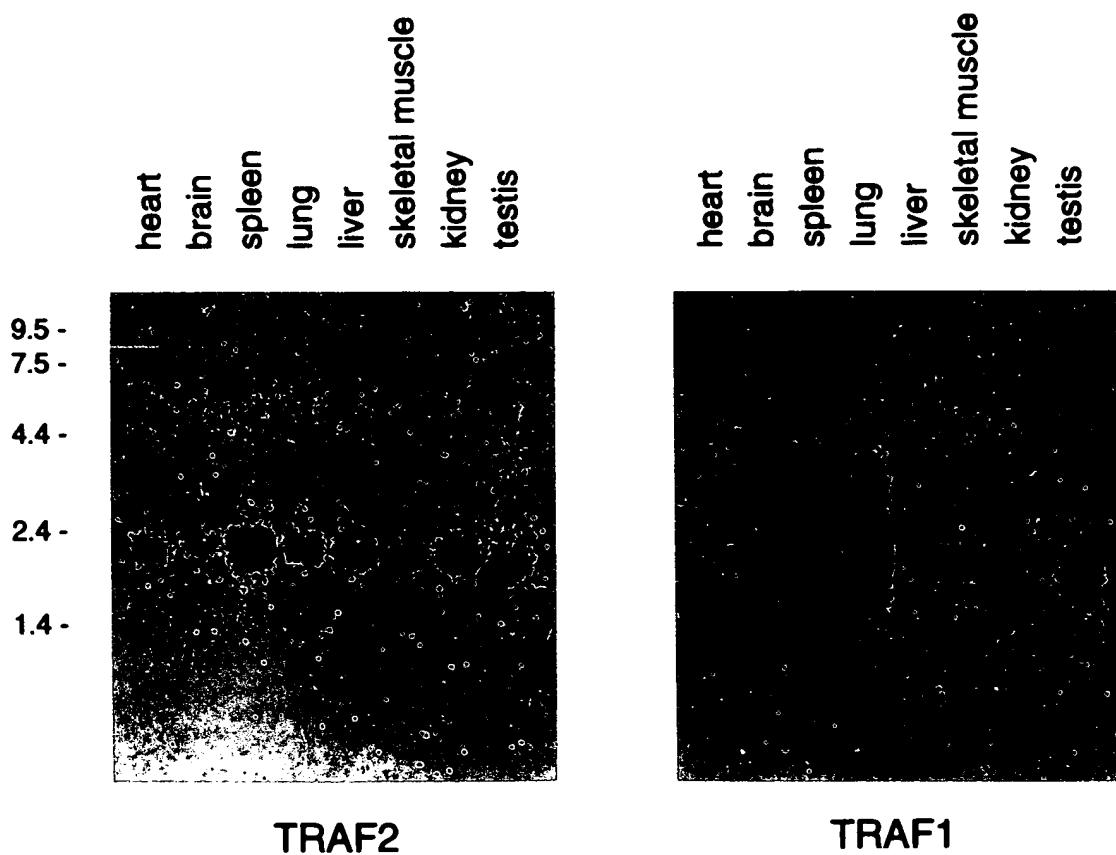


FIG. 15b

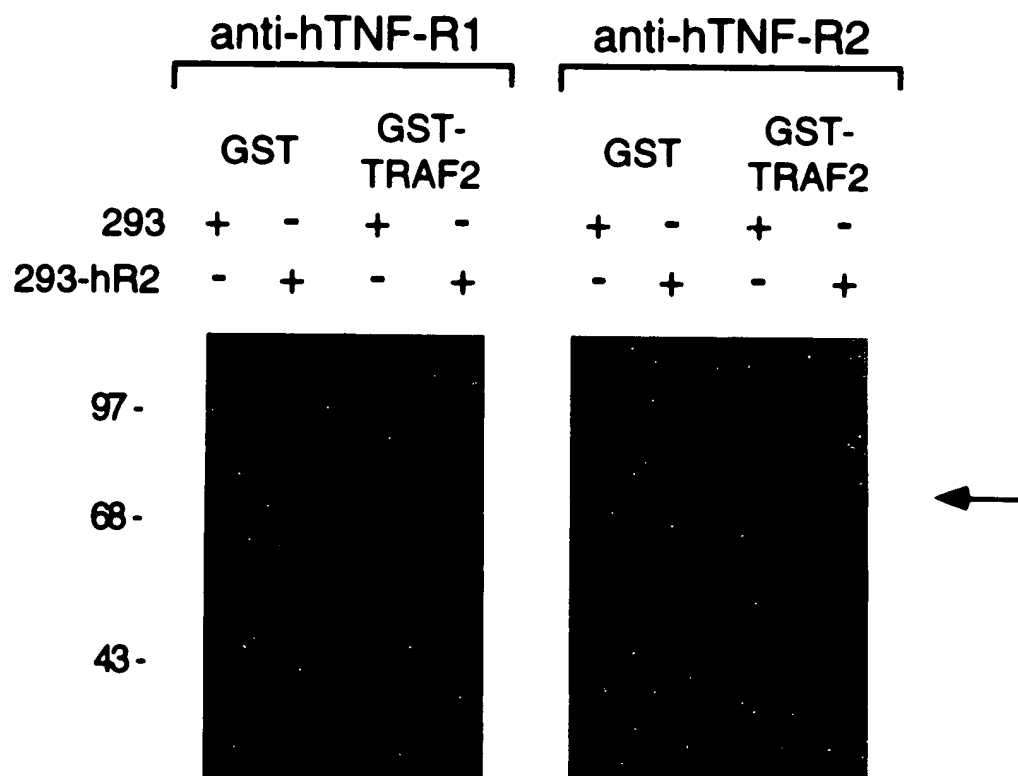


FIG. 16